

Supplementary Material

**A comparative study on the quality of protein crystals
obtained using the cross-diffusion microbatch and
sitting-drop vapor diffusion methods**

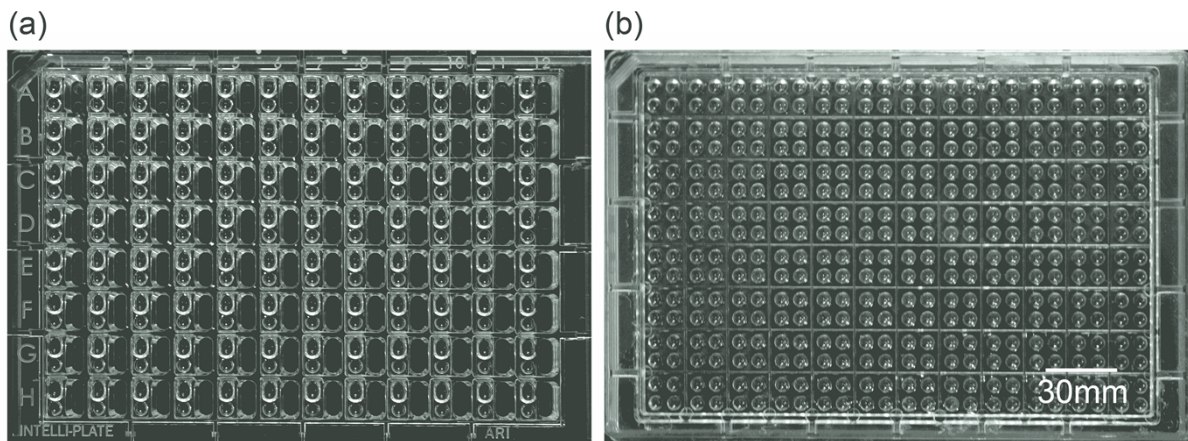
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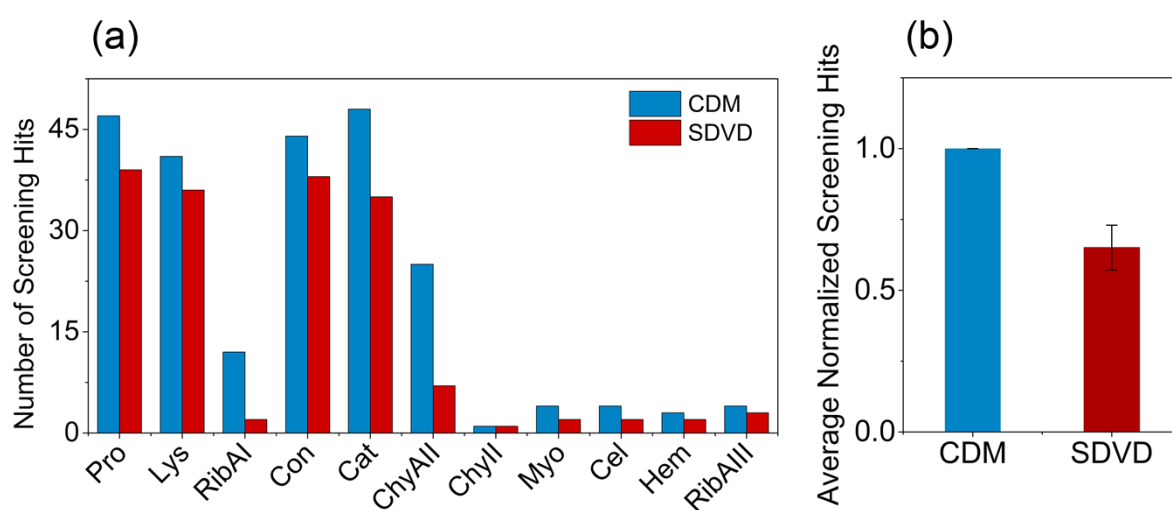
Supplementary Figure S1. Comparison of images of the crystallization plate using the CDM method and the SDVD method. (a) Image of crystallization plate using the traditional sitting

drop vapor-diffusion (SDVD) method. (b) Image of crystallization plate using the cross-diffusion microbatch (CDM) method. The size of this plate is made to be compatible with the SBS standard plate. This crystallization plate is similar to the traditional SDVD plate, except for the material and the reservoir, which was replaced by more pits to increase the number of protein concentrations or pH gradients.



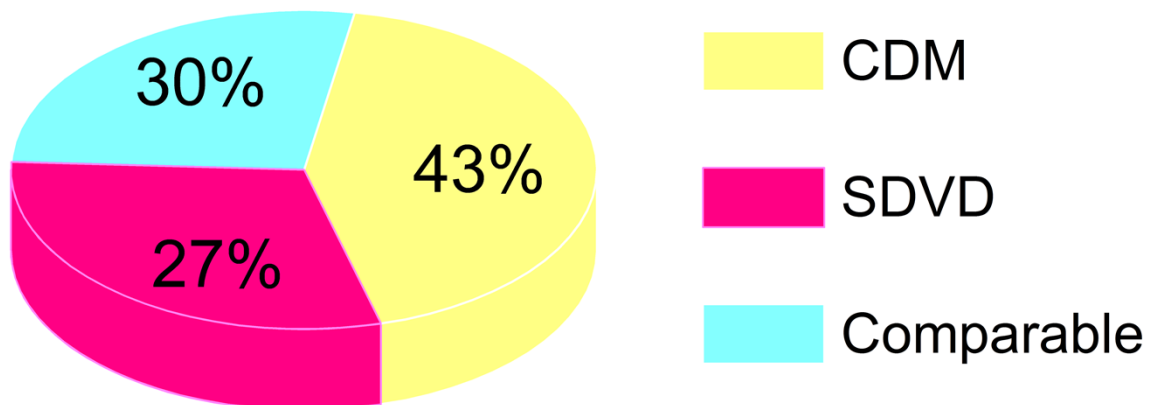
Supplementary Figure S2. (a) A comparison of crystallization screening hits for the 11 proteins using CDM and the traditional sitting drop vapor-diffusion method. (b) A statistical

analysis of the average screening hits between the CDM method and the traditional method (the error bars show the standard error of the mean; $n = 11$). The number of hits was normalized based on the data for the CDM method. The results demonstrated an extremely significant difference between the two groups ($n = 11$, $P = 0.00026$, *i.e.* <0.01). The CDM method clearly increased the number of crystallization hits compared with the traditional sitting drop vapor-diffusion method.



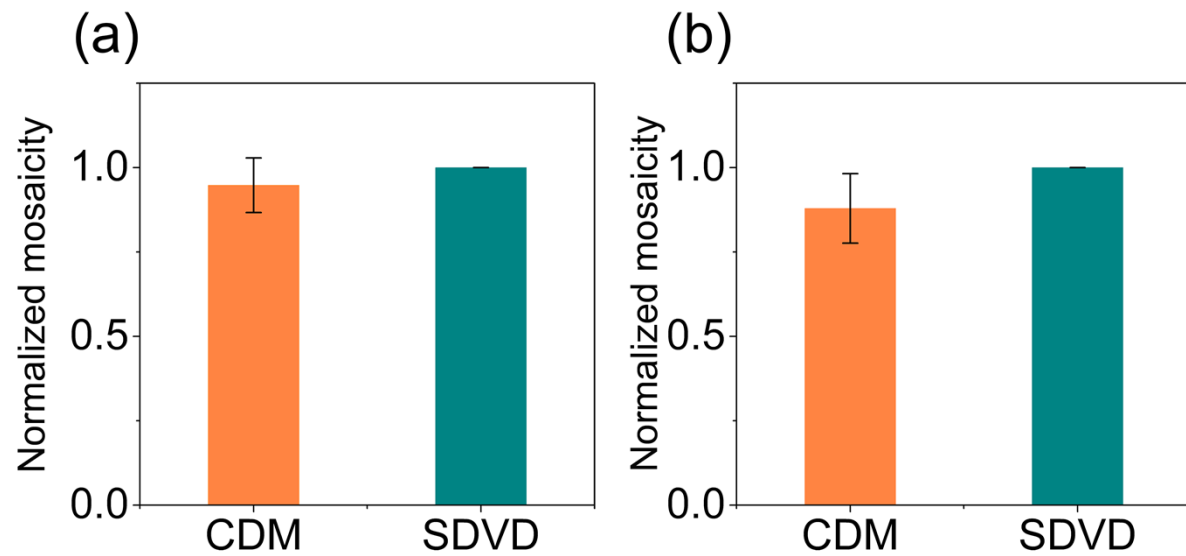
Supplementary Figure S3. Crystal morphology comparison between the CDM and SDVD crystallization plates. CDM: the crystals were optically better in the CDM plates than in the

SDVD plates. SDVD: the crystals were optically better in the SDVD plates than in the CDM plates. Comparable: the optical perfection of the crystals was comparable in the two plates. The results showed that more crystals grown in the CDM plates exhibited better optical perfection than those grown in the SDVD plates. The following criteria were used to compare the optical perfection: First, the crystals were categorized into different groups and ranked as follows: single crystal > single crystal with cracks > twin crystal > needle cluster > quasi-crystal. If the crystals were in the same group, then they were compared according to their size: larger crystals were defined as more optically perfect. If the crystal sizes were similar (size difference was within 5%), they were optically comparable.



Supplementary Figure S4. (a) A statistical comparison of the mosaicity of the top 5 proteinase K crystals after normalization. However, for mosaicity, the results demonstrated

no significant difference between the two groups ($n = 5$, $P = 0.537$, *i.e.*, >0.05). (b) A statistical comparison of the mosaicity of the top 5 lysozyme crystals after normalization. Nevertheless, for the mosaicity, the difference between the two groups was not significant ($n = 5$, $P = 0.274$, *i.e.*, >0.05).



Supplementary Table S1. X-ray diffraction data statistics of 23 proteinase K crystals in CDM crystallization plate in same size

Diffraction data statistics of proteinase K crystals in CDM crystallization plate					
□	Crystal 1	Crystal 2	Crystal 3	Crystal 4	Crystal 5
Resolution range (Å)	50-1.54 (1.57-1.54)	50-1.54 (1.57-1.54)	50-1.65 (1.68-1.65)	50-1.66 (1.69-1.66)	50-1.66 (1.69-1.66)
Mosaicity (°)	0.47	0.42	0.60	0.61	0.46
$\langle I \rangle / \langle \sigma(I) \rangle$	25.91 (7.89)	20.65 (3.39)	15.58 (2.15)	16.27 (2.76)	13.60 (2.21)
Wilson Plot B factor	6.50	8.00	7.40	9.70	7.60
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 68.17$ $b = 68.17$	$a = 67.74$ $b = 67.74$	$a = 66.52$ $b = 66.52$	$a = 68.05$ $b = 68.05$	$a = 67.75$ $b = 67.75$
a, b, c (Å)	$c = 102.13$	$c = 101.81$	$c = 99.51$	$c = 102.34$	$c = 100.56$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S1

Diffraction data statistics of proteinase K crystals in CDM crystallization plate					
☐	Crystal 6	Crystal 7	Crystal 8	Crystal 9	Crystal 10
Resolution range	50-1.66	50-1.66	50-1.66	50-1.73	50-1.76
(Å)	(1.69-1.66)	(1.69-1.66)	(1.69-1.66)	(1.76-1.73)	(1.79-1.76)
Mosaicity (°)	0.41	0.45	0.64	0.53	0.46
$\langle I \rangle / \langle \sigma(I) \rangle$	14.53 (2.44)	19.49 (4.50)	19.12 (2.70)	12.06 (2.09)	11.79 (2.04)
Wilson Plot B factor	9.90	8.40	9.80	8.30	11.10
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 67.72$	$a = 67.74$	$a = 68.02$	$a = 67.63$	$a = 67.80$
a, b, c (Å)	$b = 67.72$	$b = 67.74$	$b = 68.02$	$b = 67.63$	$b = 67.80$
α, β, γ (°)	$c = 102.26$	$c = 101.90$	$c = 101.83$	$c = 101.72$	$c = 102.34$
	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S1

Diffraction data statistics of proteinase K crystals in CDM crystallization plate					
□	Crystal 11	Crystal 12	Crystal 13	Crystal 14	Crystal 15
Resolution range	50-1.78	50-1.82	50-1.83	50-1.84	50-1.85
(Å)	(1.81-1.78)	(1.85-1.82)	(1.86-1.83)	(1.87-1.84)	(1.88-1.85)
Mosaicity (°)	0.57	0.58	0.50	0.38	0.93
$\langle I \rangle / \langle \sigma(I) \rangle$	14.93 (2.09)	13.29 (2.26)	11.54 (2.23)	9.70 (2.31)	13.96 (2.01)
Wilson Plot B factor	13.00	12.90	11.10	8.30	11.00
Space group	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2
Cell dimensions	<i>a</i> = 67.54	<i>a</i> = 67.41	<i>a</i> = 67.80	<i>a</i> = 67.72	<i>a</i> = 67.88
	<i>b</i> = 67.54	<i>b</i> = 67.41	<i>b</i> = 67.80	<i>b</i> = 67.72	<i>b</i> = 67.88
	<i>c</i> = 101.72	<i>c</i> = 100.98	<i>c</i> = 102.44	<i>c</i> = 102.22	<i>c</i> = 101.49
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S1

Diffraction data statistics of proteinase K crystals in CDM crystallization plate					
☐	Crystal 16	Crystal 17	Crystal 18	Crystal 19	Crystal 20
Resolution range	50-1.86	50-1.87	50-1.88	50-1.93	50-1.99
(Å)	(1.89-1.86)	(1.90-1.87)	(1.91-1.88)	(1.96-1.93)	(2.02-1.99)
Mosaicity (°)	1.00	0.51	0.42	0.63	0.44
$\langle I \rangle / \langle \sigma(I) \rangle$	20.22 (4.16)	10.72 (2.16)	7.95 (2.15)	14.51 (2.07)	7.91(2.01)
Wilson Plot B factor	10.30	13.00	12.80	18.60	12.00
Space group	<i>P4₃2₁2</i>	<i>P4₃2₁2</i>	<i>P4₃2₁2</i>	<i>P4₃2₁2</i>	<i>P4₃2₁2</i>
Cell dimensions	<i>a</i> = 67.99	<i>a</i> = 67.76	<i>a</i> = 67.78	<i>a</i> = 67.73	<i>a</i> = 67.77
	<i>b</i> = 67.99	<i>b</i> = 67.76	<i>b</i> = 67.78	<i>b</i> = 67.73	<i>b</i> = 67.77
	<i>c</i> = 101.83	<i>c</i> = 101.53	<i>c</i> = 102.82	<i>c</i> = 101.65	<i>c</i> = 102.51
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S1

□	Diffraction data statistics of proteinase K crystals in		
	CDM crystallization plate		
	Crystal 21	Crystal 22	Crystal 23
	50-2.17	50-2.18	50-2.20
Resolution range (Å)	(2.21-2.17)	(2.22-2.18)	(2.24-2.20)
Mosaicity (°)	0.98	0.80	0.49
$\langle I \rangle / \langle \sigma(I) \rangle$	8.40 (2.65)	7.26 (2.30)	9.06 (2.22)
Wilson Plot B factor	13.00	12.30	17.40
Space group	<i>P4₃2₁2</i>	<i>P4₃2₁2</i>	<i>P4₃2₁2</i>
Cell dimensions	<i>a</i> = 67.84	<i>a</i> = 67.87	<i>a</i> = 67.59
	<i>b</i> = 67.84	<i>b</i> = 67.87	<i>b</i> = 67.59
	<i>c</i> = 101.79	<i>c</i> = 102.21	<i>c</i> = 101.46
<i>a, b, c</i> (Å)			
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)		5	
Oscillation angle (°)		1	
Detector distance (mm)		150	
Wavelength (Å)		1.54179	

Values in parentheses are for the highest resolution shell.

Supplementary Table S2. X-ray diffraction data statistics of 20 proteinase K crystals in SDVD crystallization plate in same size

Diffraction data statistics of proteinase K crystals in SDVD crystallization plate					
□	Crystal 1	Crystal 2	Crystal 3	Crystal 4	Crystal 5
Resolution range (Å)	50-1.66 (1.69-1.66)	50-1.66 (1.69-1.66)	50-1.70 (1.70-1.73)	50-1.72 (1.75-1.72)	50-1.73 (1.76-1.73)
Mosaicity (°)	0.66	0.46	0.51	0.57	0.53
$\langle I \rangle / \langle \sigma(I) \rangle$	20.96 (3.32)	17.63 (2.70)	13.45 (2.04)	13.65 (2.13)	11.92 (2.19)
Wilson Plot B factor	13.30	11.50	11.90	10.40	11.00
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 68.10$ $b = 68.10$	$a = 68.12$ $b = 68.12$	$a = 67.93$ $b = 67.93$	$a = 67.82$ $b = 67.82$	$a = 67.43$ $b = 67.43$
a, b, c (Å)	$c = 101.90$	$c = 102.33$	$c = 101.62$	$c = 101.41$	$c = 101.00$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S2

Diffraction data statistics of proteinase K crystals in SDVD crystallization plate					
☐	Crystal 6	Crystal 7	Crystal 8	Crystal 9	Crystal 10
Resolution range	50-1.77	50-1.78	50-1.85	50-1.86	50-1.87
(Å)	(1.80-1.77)	(1.81-1.78)	(1.88-1.85)	(1.89-1.86)	(1.90-1.87)
Mosaicity (°)	0.79	0.75	1.28	0.78	0.61
$\langle I \rangle / \langle \sigma(I) \rangle$	14.45 (2.07)	13.07 (2.08)	10.34 (3.63)	17.62 (2.58)	7.85 (2.07)
Wilson Plot B factor	11.30	12.40	10.60	14.40	19.60
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 68.19$	$a = 67.72$	$a = 67.90$	$a = 67.32$	$a = 67.98$
	$b = 68.19$	$b = 67.72$	$b = 67.90$	$b = 67.32$	$b = 67.98$
	$c = 102.04$	$c = 100.50$	$c = 95.15$	$c = 102.17$	$c = 101.88$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S2

Diffraction data statistics of proteinase K crystals in SDVD crystallization plate					
☐	Crystal 11	Crystal 12	Crystal 13	Crystal 14	Crystal 15
Resolution range	50-1.95	50-1.98	50-2.05	50-2.08	50-2.09
(Å)	(1.98-1.95)	(2.01-1.98)	(2.09-2.05)	(2.12-2.08)	(2.13-2.09)
Mosaicity (°)	0.69	1.39	0.83	1.12	1.61
$\langle I \rangle / \langle \sigma(I) \rangle$	9.58 (2.07)	11.82 (2.33)	6.10 (2.04)	10.85 (2.17)	11.18 (2.13)
Wilson Plot B factor	11.60	18.30	15.90	16.40	10.10
Space group	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2
Cell dimensions	<i>a</i> = 67.75	<i>a</i> = 67.75	<i>a</i> = 67.95	<i>a</i> = 66.66	<i>a</i> = 67.59
<i>a</i> , <i>b</i> , <i>c</i> (Å)	<i>b</i> = 67.75	<i>b</i> = 67.75	<i>b</i> = 67.95	<i>b</i> = 66.66	<i>b</i> = 67.59
α , β , γ (°)	<i>c</i> = 101.21	<i>c</i> = 101.58	<i>c</i> = 101.61	<i>c</i> = 100.10	<i>c</i> = 100.84
Exposure time (min)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Oscillation angle (°)			5		
Detector distance (mm)			1		
Wavelength (Å)			150		
			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S2

Diffraction data statistics of proteinase K crystals in SDVD crystallization plate					
☐	Crystal 16	Crystal 17	Crystal 18	Crystal 19	Crystal 20
Resolution range	50-2.11	50-2.20	50-2.38	50-2.78	50-3.07
(Å)	(2.15-2.11)	(2.24-2.20)	(2.42-2.38)	(2.83-2.78)	(3.12-3.07)
Mosaicity (°)	0.81	0.47	0.39	0.38	0.48
$\langle I \rangle / \langle \sigma(I) \rangle$	9.62 (7.99)	5.14 (2.09)	5.34 (2.40)	5.09 (2.31)	3.96 (2.96)
Wilson Plot B factor	17.70	17.70	17.30	16.00	21.20
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 68.03$	$a = 67.72$	$a = 67.84$	$a = 67.73$	$a = 67.69$
a, b, c (Å)	$b = 68.03$	$b = 67.72$	$b = 67.84$	$b = 67.73$	$b = 67.69$
α, β, γ (°)	$c = 102.80$	$c = 102.11$	$c = 102.63$	$c = 102.59$	$c = 102.37$
	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Supplementary Table S3. X-ray diffraction data statistics of 27 lysozyme crystals in CDM crystallization plate in same size

Diffraction data statistics of lysozyme crystals in CDM crystallization plate					
□	Crystal 1	Crystal 2	Crystal 3	Crystal 4	Crystal 5
Resolution range (Å)	50-1.66	50-1.66	50-1.78	50-1.83	50-1.86
	(1.69-1.66)	(1.69-1.66)	(1.81-1.78)	(1.86-1.83)	(1.89-1.86)
Mosaicity (°)	0.60	0.57	0.83	0.52	0.74
$\langle I \rangle / \langle \sigma(I) \rangle$	23.18 (8.58)	24.29 (2.11)	21.92 (2.24)	15.85 (2.02)	19.98 (2.12)
Wilson Plot B factor	16.40	14.00	18.20	19.40	14.10
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 76.91$	$a = 78.22$	$a = 78.02$	$a = 76.47$	$a = 76.71$
	$b = 76.91$	$b = 78.22$	$b = 78.02$	$b = 76.47$	$b = 76.71$
a, b, c (Å)	$c = 38.35$	$c = 37.62$	$c = 37.55$	$c = 37.58$	$c = 37.32$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S3

Diffraction data statistics of lysozyme crystals in CDM crystallization plate					
☐	Crystal 6	Crystal 7	Crystal 8	Crystal 9	Crystal 10
Resolution range	50-1.86	50-1.86	50-1.86	50-1.86	50-1.86
(Å)	(1.89-1.86)	(1.89-1.86)	(1.89-1.86)	(1.89-1.86)	(1.89-1.86)
Mosaicity (°)	0.59	0.82	0.84	0.89	0.52
$\langle I \rangle / \langle \sigma(I) \rangle$	18.70 (3.34)	18.75 (2.12)	15.50 (3.05)	22.0 (2.46)	12.93 (3.67)
Wilson Plot B factor	18.90	15.00	14.70	16.90	20.70
Space group	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2
Cell dimensions	<i>a</i> = 76.80	<i>a</i> = 76.47	<i>a</i> = 76.91	<i>a</i> = 76.77	<i>a</i> = 76.82
<i>a</i> , <i>b</i> , <i>c</i> (Å)	<i>b</i> = 76.80	<i>b</i> = 76.47	<i>b</i> = 76.91	<i>b</i> = 76.77	<i>b</i> = 76.82
α , β , γ (°)	<i>c</i> = 37.35	<i>c</i> = 37.58	<i>c</i> = 37.74	<i>c</i> = 37.27	<i>c</i> = 37.39
	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S3

Diffraction data statistics of lysozyme crystals in CDM crystallization plate					
☐	Crystal 11	Crystal 12	Crystal 13	Crystal 14	Crystal 15
Resolution range	50-1.87	50-1.92	50-1.93	50-1.94	50-1.94
(Å)	(1.90-1.87)	(1.95-1.92)	(1.96-1.93)	(1.97-1.94)	(1.97-1.94)
Mosaicity (°)	0.83	1.03	0.50	0.86	0.86
$\langle I \rangle / \langle \sigma(I) \rangle$	17.73 (2.89)	16.84 (2.44)	10.85 (2.02)	18.37 (2.145)	14.36 (2.56)
Wilson Plot B factor	22.20	20.20	21.40	25.30	24.10
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 77.24$	$a = 76.57$	$a = 76.67$	$a = 77.27$	$a = 76.43$
a, b, c (Å)	$b = 77.24$	$b = 76.57$	$b = 76.67$	$b = 77.27$	$b = 76.43$
α, β, γ (°)	$c = 37.81$	$c = 37.08$	$c = 37.20$	$c = 37.07$	$c = 36.74$
	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S3

Diffraction data statistics of lysozyme crystals in CDM crystallization plate					
□	Crystal 16	Crystal 17	Crystal 18	Crystal 19	Crystal 20
	50-2.02	50-2.03	50-2.08	50-2.09	50-2.10
Resolution range (Å)	(2.05-2.02)	(2.06-2.03)	(2.12-2.08)	(2.13-2.09)	(2.14-2.10)
Mosaicity (°)	1.08	0.61	0.52	1.01	0.70
$\langle I \rangle / \langle \sigma(I) \rangle$	14.49 (2.30)	18.16 (3.23)	13.86 (2.14)	17.36 (2.01)	21.14 (2.30)
Wilson Plot B factor	14.70	23.20	23.60	19.20	21.40
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 77.00$	$a = 78.30$	$a = 77.29$	$a = 76.09$	$a = 78.79$
	$b = 77.00$	$b = 78.30$	$b = 77.29$	$b = 76.09$	$b = 78.79$
	$c = 37.70$	$c = 35.93$	$c = 37.04$	$c = 37.17$	$c = 35.41$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S3

Diffraction data statistics of lysozyme crystals in CDM crystallization plate					
☐	Crystal 21	Crystal 22	Crystal 23	Crystal 24	Crystal 25
Resolution range	50-2.12	50-2.12	50-2.21	50-2.23	50-2.23
(Å)	(2.16-2.12)	(2.16-2.12)	(2.25-2.21)	(2.27-2.23)	(2.27-2.23)
Mosaicity (°)	1.03	1.18	0.96	0.62	0.62
$\langle I \rangle / \langle \sigma(I) \rangle$	15.56 (2.17)	24.25 (2.38)	22.49 (8.30)	10.32 (2.09)	11.40 (2.35)
Wilson Plot B factor	21.40	22.60	19.80	27.10	25.40
Space group	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2
Cell dimensions	<i>a</i> = 75.72	<i>a</i> = 76.12	<i>a</i> = 77.99	<i>a</i> = 76.66	<i>a</i> = 77.66
	<i>b</i> = 75.72	<i>b</i> = 76.12	<i>b</i> = 77.99	<i>b</i> = 76.66	<i>b</i> = 77.66
	<i>c</i> = 36.83	<i>c</i> = 37.18	<i>c</i> = 36.86	<i>c</i> = 37.51	<i>c</i> = 37.46
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S3

□	Diffraction data statistics of lysozyme crystals in CDM crystallization plate	
	Crystal 26	Crystal 27
Resolution range (Å)	50-2.38 (2.42-2.38)	50-2.72 (2.77-2.72)
Mosaicity (°)	0.99	0.58
$\langle I \rangle / \langle \sigma(I) \rangle$	16.68 (2.72)	6.29 (2.56)
Wilson Plot B factor	27.10	25.40
Space group	$P4_32_12$	$P4_32_12$
Cell dimensions a, b, c (Å)	$a = 78.45$	$a = 76.83$
	$b = 78.45$	$b = 76.83$
	$c = 36.21$	$c = 37.11$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)		5
Oscillation angle (°)		1
Detector distance (mm)		150
Wavelength (Å)		1.54179

Values in parentheses are for the highest resolution shell.

Supplementary Table S4. X-ray diffraction data statistics of 23 lysozyme crystals in SDVD crystallization plate in same size

Diffraction data statistics of lysozyme crystals in SDVD crystallization plate					
□	Crystal 1	Crystal 2	Crystal 3	Crystal 4	Crystal 5
Resolution range (Å)	50-1.86 (1.89-1.86)	50-1.86 (1.89-1.86)	50-1.88 (1.91-1.88)	50-1.88 (1.91-1.88)	50-1.91 (1.94-1.91)
Mosaicity (°)	0.61	0.91	0.75	0.82	0.71
$\langle I \rangle / \langle \sigma(I) \rangle$	18.51 (2.04)	15.43 (2.49)	11.83 (2.70)	13.74 (2.13)	14.69 (2.01)
Wilson Plot B factor	18.60	18.60	24.90	28.30	22.90
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 78.49$ $b = 78.49$	$a = 77.36$ $b = 77.36$	$a = 75.79$ $b = 75.79$	$a = 77.78$ $b = 77.78$	$a = 76.30$ $b = 76.30$
a, b, c (Å)	$c = 37.21$	$c = 37.52$	$c = 36.61$	$c = 37.54$	$c = 36.65$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S4

Diffraction data statistics of lysozyme crystals in SDVD crystallization plate					
☐	Crystal 6	Crystal 7	Crystal 8	Crystal 9	Crystal 10
Resolution range	50-1.93	50-2.00	50-2.02	50-2.03	50-2.03
(Å)	(1.96-1.93)	(2.03-2.00)	(2.05-2.02)	(2.06-2.03)	(2.06-2.03)
Mosaicity (°)	0.85	0.95	0.60	0.54	0.94
$\langle I \rangle / \langle \sigma(I) \rangle$	10.35 (2.33)	21.78 (2.37)	13.51 (2.07)	13.10 (2.02)	15.47 (2.68)
Wilson Plot B factor	20.60	20.10	23.70	21.90	22.60
Space group	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2	<i>P</i> 4 ₃ 2 ₁ 2
Cell dimensions	<i>a</i> = 78.73	<i>a</i> = 78.87	<i>a</i> = 76.99	<i>a</i> = 77.97	<i>a</i> = 77.69
<i>a</i> , <i>b</i> , <i>c</i> (Å)	<i>b</i> = 78.73	<i>b</i> = 78.87	<i>b</i> = 76.99	<i>b</i> = 77.97	<i>b</i> = 77.69
	<i>c</i> = 37.99	<i>c</i> = 37.26	<i>c</i> = 37.11	<i>c</i> = 37.85	<i>c</i> = 37.85
α , β , γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S4

Diffraction data statistics of lysozyme crystals in SDVD crystallization plate					
☐	Crystal 11	Crystal 12	Crystal 13	Crystal 14	Crystal 15
Resolution range	50-2.08	50-2.10	50-2.12	50-2.15	50-2.24
(Å)	(2.12-2.08)	(2.14-2.10)	(2.16-2.12)	(2.19-2.15)	(2.28-2.24)
Mosaicity (°)	1.32	1.89	0.92	0.96	1.38
$\langle I \rangle / \langle \sigma(I) \rangle$	12.22 (3.18)	15.39 (6.07)	12.25 (2.26)	18.89 (5.41)	16.04 (2.48)
Wilson Plot B factor	23.50	12.80	22.00	21.80	26.00
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 76.44$	$a = 76.50$	$a = 75.87$	$a = 78.02$	$a = 79.00$
a, b, c (Å)	$b = 76.44$	$b = 76.50$	$b = 75.87$	$b = 78.02$	$b = 79.00$
α, β, γ (°)	$c = 36.73$	$c = 37.62$	$c = 37.73$	$c = 37.48$	$c = 35.94$
	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S4

Diffraction data statistics of lysozyme crystals in SDVD crystallization plate					
☐	Crystal 16	Crystal 17	Crystal 18	Crystal 19	Crystal 20
Resolution range	50-2.26	50-2.28	50-2.45	50-2.51	50-2.61
(Å)	(2.30-2.26)	(2.32-2.28)	(2.49-2.45)	(2.55-2.51)	(2.66-2.61)
Mosaicity (°)	1.04	1.12	0.74	0.85	1.45
$\langle I \rangle / \langle \sigma(I) \rangle$	10.16 (3.49)	18.87 (2.69)	9.40 (2.05)	12.20 (2.78)	7.11 (3.35)
Wilson Plot B factor	24.40	24.40	27.40	28.50	32.90
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 76.48$	$a = 75.70$	$a = 76.90$	$a = 76.01$	$a = 76.54$
	$b = 76.48$	$b = 75.70$	$b = 76.90$	$b = 76.01$	$b = 76.54$
	$c = 37.01$	$c = 36.21$	$c = 37.50$	$c = 37.01$	$c = 36.97$
α, β, γ (°)	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)			5		
Oscillation angle (°)			1		
Detector distance (mm)			150		
Wavelength (Å)			1.54179		

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S4

□	Diffraction data statistics of lysozyme crystals in SDVD		
	crystallization plate		
	Crystal 21	Crystal 22	Crystal 23
Resolution range (Å)	50-2.80 (2.85-2.80)	50-3.25 (3.31-3.25)	50-3.45 (3.51-3.45)
Mosaicity (°)	0.95	1.48	1.45
$\langle I \rangle / \langle \sigma(I) \rangle$	13.61 (2.62)	10.31 (73.05)	10.51 (2.34)
Wilson Plot B factor	30.90	31.20	29.80
Space group	$P4_32_12$	$P4_32_12$	$P4_32_12$
Cell dimensions	$a = 75.73$	$a = 75.54$	$a = 76.08$
a, b, c (Å)	$b = 75.73$	$b = 75.54$	$b = 76.08$
α, β, γ (°)	$c = 36.49$	$c = 36.54$	$c = 37.30$
	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$	$\alpha = \beta = \gamma = 90$
Exposure time (min)		5	
Oscillation angle (°)		1	
Detector distance (mm)		150	
Wavelength (Å)		1.54179	

Values in parentheses are for the highest resolution shell.

Supplementary Table S5. X-ray diffraction data statistics of 8 ribonuclease A I crystals in CDM crystallization plate in same size

Diffraction data statistics of ribonuclease A I crystals in CDM crystallization plate					
□	Crystal 1	Crystal 2	Crystal 3	Crystal 4	Crystal 5
Resolution range	50-1.84	50-2.33	50-2.69	50-2.88	50-2.88
(Å)	(1.87-1.84)	(2.37-2.33)	(2.74-2.69)	(2.93-2.88)	(2.93-2.88)
Mosaicity (°)	0.95	1.29	1.85	1.28	1.04
$\langle I \rangle / \langle \sigma(I) \rangle$	13.31 (5.0)	13.37 (2.51)	9.29 (2.01)	9.80 (3.45)	7.36 (3.33)
Wilson Plot B factor	13.40	33.40	20.30	24.00	21.20
Space group	<i>P</i> 6 ₂ 22	<i>P</i> 6 ₂ 22	<i>P</i> 6 ₂ 22	<i>P</i> 6 ₂ 22	<i>P</i> 6 ₂ 22
Cell dimensions	<i>a</i> = 63.63	<i>a</i> = 64.02	<i>a</i> = 66.16	<i>a</i> = 63.68	<i>a</i> = 63.59
<i>a, b, c</i> (Å)	<i>b</i> = 63.63	<i>b</i> = 64.02	<i>b</i> = 66.16	<i>b</i> = 63.68	<i>b</i> = 63.59
α, β, γ (°)	<i>c</i> = 63.35	<i>c</i> = 64.21	<i>c</i> = 69.54	<i>c</i> = 64.36	<i>c</i> = 64.49
	$\alpha = \beta = 90$	$\alpha = \beta = 90$	$\alpha = \beta = 90$	$\alpha = \beta = 90$	$\alpha = \beta = 90$
	$\gamma = 120$	$\gamma = 120$	$\gamma = 120$	$\gamma = 120$	$\gamma = 120$
Exposure time (min)			10		
Oscillation angle (°)			1		
Detector distance			150		

(mm)

Wavelength (Å) 1.54179

Values in parentheses are for the highest resolution shell.

Continued Supplementary Table S5

□	Diffraction data statistics of ribonuclease A I crystals in		
	CDM crystallization plate		
	Crystal 6	Crystal 7	Crystal 8
Resolution range	50-3.16	50-3.18	50-3.52
(Å)	(3.21-3.16)	(3.23-3.18)	(3.58-3.52)
Mosaicity (°)	1.36	1.28	2.28
$\langle I \rangle / \langle \sigma(I) \rangle$	5.88 (2.07)	7.26 (2.13)	6.26 (2.36)
Wilson Plot B factor	28.10	30.80	33.00
Space group	<i>P</i> 6 ₂ 22	<i>P</i> 6 ₂ 22	<i>P</i> 6 ₂ 22
Cell dimensions	<i>a</i> = 63.51	<i>a</i> = 63.61	<i>a</i> = 64.91
	<i>b</i> = 63.51	<i>b</i> = 63.61	<i>b</i> = 64.91
	<i>a, b, c</i> (Å)	<i>c</i> = 63.41	<i>c</i> = 64.08
α, β, γ (°)	$\alpha = \beta = 90$	$\alpha = \beta = 90$	$\alpha = \beta = 90$
	$\gamma = 120$	$\gamma = 120$	$\gamma = 120$
Exposure time (min)	10		

Oscillation angle (°)	1
Detector distance (mm)	150
Wavelength (Å)	1.54179

Values in parentheses are for the highest resolution shell.

Supplementary Table S6. The number of droplets containing amorphous precipitate in CDM and SDVD crystallization plates for the 11 different proteins.

Protein	Number of amorphous precipitate conditions	
	CDM	SDVD
Proteinase K	15	11
Lysozyme	19	16
Ribonuclease A I	5	0
Concanavalin A VI	17	12
Catalase	13	11
α -chymotrypsinogen A II	9	2
α -chymotrypsin II	14	10
Myoglobin	8	11
Cellulase	6	4
Hemoglobin	12	7
Ribonuclease A III	10	3
